

Cyanobacteria. Credit: L. Prufert-Bebout

Exobiology Branch (SSX) Overview

The Branch's research focuses on the advancement of the scientific understanding of the origin and distribution of life by conducting research on the cosmic history of biogenic compounds, prebiotic evolution, and the early evolution of life. This is accomplished via laboratory experiments, theoretical studies/computational modeling, and field investigations. Branch personnel are also involved in the development of flight instruments, experiments, and small mission definition with particular emphasis being placed on studies of Mars and the development of instrumentation for martian flight missions. Several Branch scientists are part of a task module that is a component of the Ames membership in the Astrobiology Institute. Branch scientists provide expertise in exobiology, astrobiology, planetary protection, and other areas of planetary science to NASA Headquarters and external review and advisory panels, and some serve as editors and associate editors of scientific journals.

Exobiology studies includes the history, distribution, and chemistry of biogenic elements in the solar system; prebiotic chemical evolution and the origin of life; and the history of Earth's early biosphere as recorded in microorganisms and ancient rocks. The research is conducted both on Earth and in space. The Branch also serves as the center of expertise within the agency for issues of planetary protection. As the agency lead center in exobiology, Branch exobiologists exercise a leadership role in NASA's Exobiology Program through program planning, performance reviews, advisory services to related NASA programs, and external relations.

David F. Blake

Chief, Exobiology Branch (SSX)

EMERG GREENHOUSE ONE: SIMULATIONS OF REMOTE AND ANCIENT EARTH ENVIRONMENTS AT AMES

Brad Bebout

The Ames Microbial Ecology/Biogeochemistry Research Lab, in combination with the Early Microbial Ecosystems Research Group (EMERG), has completed a greenhouse simulation facility designed to enable the maintenance and manipulation of microbial mat communities. Microbial mat communities are extant representatives of the oldest forms of life on Earth. Two major experiments, a salinity manipulation, and a sulfate manipulation, have now been conducted. These experiments have demonstrated that the facility is capable of maintaining these complex communities of microorganisms for periods of over a year, while enabling experimental manipulations and the collection of high quality data. The experimental apparatus notably enables the collection of measurements of the distribution of important chemical and biological parameters within the communities on the microscale (sub millimeter).

The salinity manipulation, in which the salinity of half of the experimental microbial mats was raised by a factor of about 30 per cent, provided the important result that the community composition of the major photosynthetic population in the mats (cyanobacteria), as revealed using molecular biological methods, is essentially identical to that of field collected populations. Increased salinity reproduced cyanobacterial community changes that are also observed with increases in salinity in the natural environment. The importance of this result is a validation of the methods being using to conduct manipulations.

The sulfate manipulation, in which the sulfate concentrations of half of the experimental mats was reduced by a factor of nearly 1000, recreates conditions which were important early in Earth's history, but which are not presently found in the natural environment. This manipulation has produced a number of fundamental changes in the microbial mats, including changes in sulfate reduction, oxygen distribution within the mat, and photosynthetic efficiency. In addition, changes in important biomarker gases were observed between the treatments, including higher rates of methane and dimethyl sulfide production in mats incubated at lower sulfate concentrations. These results will be important in evaluating the strategy of looking at biomarker gases in the atmospheres of extrasolar planets. □

A TERRESTRIAL ANALOG FOR THE MARTIAN METEORITE ALH84001

David Blake, Allan H. Treiman, Hans E.F. Amundsen and Ted Bunch

Carbonate minerals present in the ancient Mars meteorite ALH84001 may hold clues to the processing and fate of volatiles and the potential for primitive life on early Mars. However, because ALH84001 is separated from its surrounding rocks, the context of its formation and processing is unknown and the origin of the carbonate globules has therefore been controversial — scenarios range from groundwater deposition through high-temperature shock metamorphism. In terrestrial field geology, such rocks are called “float” when they are found removed from their original setting. The ALH84001 meteorite is an extreme example of “float”, having been separated from its source locality (Mars) by hundreds of millions of miles.

One way to investigate the origin of rocks whose context to the surrounding strata has been lost is to find and study analogous rocks where field relationships can be obtained. Igneous rocks from volcanoes on northern Spitsbergen (Svalbard, Norway) contain carbonate globules strikingly similar to the globules in ALH84001 (see Figure 15). Field and laboratory data suggest that the Spitzbergen carbonates formed as a result of late-stage hydrothermal (i.e., hot springs) activity. The ALH84001 carbonates probably formed in a similar environment.

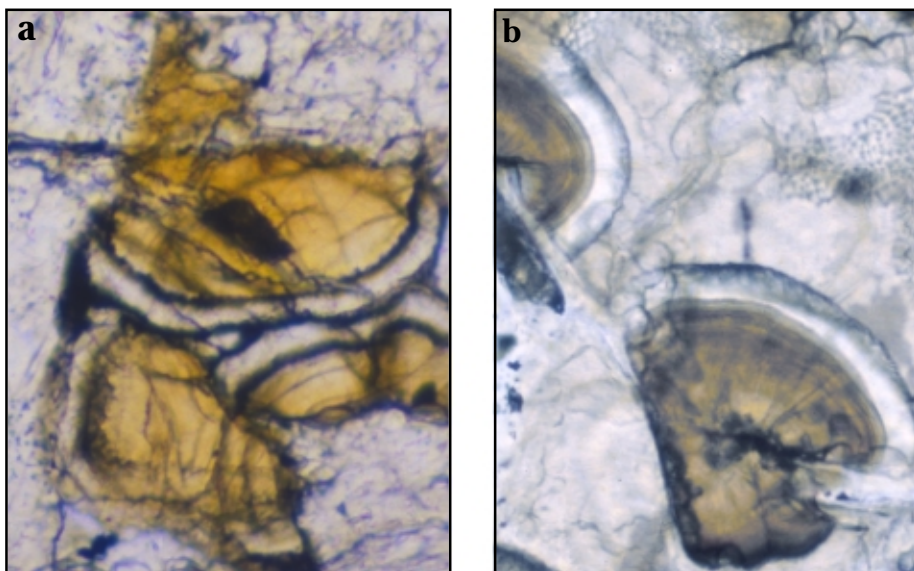


Figure 15: Optical microscope views of carbonate globules from Mars and Earth. Semicircular globules, ~ 200 μm diameter, have cores of ankerite and siderite carbonates (brown, Fe- and Ca-rich), and rims of magnesite (clear, Mg-rich) [a] Mars. Meteorite ALH84001. Black layers are magnetite-rich (originally were siderite, Fe-rich carbonate). Globules surrounded by orthopyroxene and feldspathic glass. [b] Earth. Spitsbergen xenolith, sequence of carbonate minerals similar to ALH84001 globule. Globules surrounded by olivine, orthopyroxene, clay, and silica; globules cut by clay-filled veinlets.

Xenoliths (rock fragments dislodged and entrained in rising magma) comprise up to 20% of the exposed volumes of basalt from several volcanos on Spitsbergen. The mantle xenoliths within the basalt include rock types similar to ALH84001. Globules of carbonate minerals occur in the xenoliths and their host lavas along cracks, in vesicles, and as replacements of olivine. Typical carbonate globules in the Spitsbergen rocks are ellipsoids cored by ankerite, siderite, and magnesite (ASM), carbonate minerals also present in ALH84001.

Results suggest that the ASM carbonates were deposited *in situ*, in restricted areas, in the volcanic centers by hydrothermal fluids. The ASM carbonate globules from the Spitsbergen volcanos are similar to the carbonate globules in ALH84001, having similar sizes, shapes, chemical compositions, general patterns of chemical zoning, and host rock compositions. These similarities suggest that the Spitsbergen and ALH84001 carbonate masses formed in comparable geological environments.

The current focus of Mars exploration is water and ancient environments where life may have prospered, including hydrothermal systems. The ALH84001 carbonates are critical to this search, almost by default, as they are our only direct clues about ancient Martian aqueous environments and geochemistry. Further study of the Spitsbergen rocks will help clarify the formation conditions for the carbonates, provide a sound terrestrial basis for interpreting the carbonates in ALH84001, and aid in planning geological and geochemical studies of the Martian highlands. □

MICROBIAL MATS AND THE ORIGINS OF PHOTOSYNTHESIS

David Des Marais, Dan Albert, Brad Bebout, Mykell Discipulo, Tori Hoehler, and Kendra Turk

The Ames microbial ecology laboratory (EMERG) is defining the structure and function of microbial biofilm (mat) communities. Recent observations of aerobic and anaerobic processes within these communities offer clues about our earliest origins and about the nature of Earth's ancient atmosphere. Such studies contribute directly to NASA missions that seek to chart the distribution of habitable planets and biospheres beyond Earth.

When our biosphere developed photosynthesis, probably in microbial mats, it tapped an energy resource that was orders of magnitude larger than the energy available from oxidation-reduction reactions associated with weathering and hydrothermal activity. The onset of oxygenic photosynthesis most probably increased global organic productivity by more than two orders of magnitude. This productivity materialized principally because oxygenic photosynthetic bacteria can capture hydrogen for organic biosynthesis by cleaving the water molecule. This virtually unlimited supply of reduced hydrogen forever freed life from its sole dependence upon abiotic sources of reducing power such as hydrothermal emanations and weathering. Communities sustained by oxygenic photosynthesis thrived wherever supplies of sunlight, moisture and nutrients were sufficient. The microfossil record

of cyanobacteria is evident for more than 2.5 billion years, and their ancient stromatolitic reefs rival modern reefs in size. Vast sedimentary deposits of organic carbon, reduced sulfide, and ferric iron on continental platforms and margins are among the most prominent and enduring legacies of billions of years of oxygenic photosynthetic activity. The biosphere passed through an earlier stage where even its photosynthetic populations depended exclusively upon nonbiological sources of reducing power from hydrothermal emanations and rock weathering. Can we recognize such a stage? In order to chart the development of oxygenic photosynthesis as well as its impact upon the atmosphere and ancient sediments, it is important to learn how to discriminate between the fossil remains of aerobic versus anaerobic populations.

The Ames team examined modern descendants of these ancient mats in subtidal and intertidal marine environments at Guerrero Negro, BCS, Mexico, specifically those dominated by *Microcoleus* (subtidal) and *Lyngbya* (intertidal to supratidal) cyanobacteria. Differences in the aerobic versus anaerobic communities were observed that indeed might be preserved in the sedimentary record. The exchange of O₂ and dissolved inorganic C (DIC) between mats and the overlying water, during diel (24hr.) cycles. *Microcoleus* mats assimilated near-equal amounts of DIC during the day as they released at night, but *Lyngbya* mats typically showed net uptake of DIC over the diel cycle. Patterns of O₂ daytime release and nighttime uptake mirrored these DIC trends in both mat types. Nighttime DIC effluxes from *Microcoleus* mats were equivalent in the presence versus absence of O₂, whereas nighttime DIC effluxes from *Lyngbya* mats dropped markedly in the absence of O₂. Thus, aerobic diagenesis was more important in *Lyngbya* mats than in *Microcoleus* mats, perhaps because trapped O₂ bubbles persist only in *Lyngbya* mats at night and thus sustain populations of aerobes. In both mat types, effluxes of H₂, CH₄ and short-chain fatty acids were much greater at night in the absence of O₂, emphasizing the importance of fermentation reactions. Differences observed between *Microcoleus* versus *Lyngbya* mats forecast differences in their microbiota and in their patterns of gene expression. □

LARGE-MAGNITUDE BIOLOGICAL INPUT OF HYDROGEN TO THE ARCHAEOAN ATMOSPHERE

Tori M. Hoehler, Brad M. Bebout, and David J. DesMarais

Earth's earliest biosphere is often thought to have depended primarily on chemicals vented from deep underground (as in volcanoes or hydrothermal vents) as its primary source of energy. Before long, however, life "learned" how to use solar radiation (light) as the primary energy source. Because light provides a much more abundant supply of energy, the new photosynthetic biosphere had the potential to be more productive than the earlier biosphere by as much as two or three orders of magnitude. Accordingly, the capacity of life to alter the chemistry of our planet's surface must have increased by a similar magnitude. The Early Microbial Ecosystems Research Group (EMERG) at Ames Research Center is studying modern relatives of Earth's ancient photosynthetic biosphere in order to understand the possible biological impacts on planetary chemistry during the early stages of our history.

Some of our recent studies have focused on the production of hydrogen gas, H_2 , by modern microbial mats (analogues for ancient photosynthetic communities). During photosynthesis, microbial mats break water, H_2O , into its component elements of hydrogen and oxygen. Ordinarily, the H_2 is used to turn carbon dioxide from the atmosphere into sugar-like materials – which are subsequently used to synthesize the complex organic molecules that comprise living organisms. However, when microbial mats are exposed to a simulated Archaean (early Earth) atmosphere that is very low in oxygen, they instead release much of this hydrogen to the environment. Without this mechanism, the primary source of H_2 to the Archaean atmosphere would have been geothermal venting (e.g., volcanic emissions); our studies suggest the biological release of hydrogen may have exceeded the geological one by 100 to 10,000 times.

Such a profound addition of hydrogen to the Archaean environment could have had important implications for both biology and chemistry on a global scale. Hydrogen is widely utilized as a food source by many of the organisms thought to have comprised the early biosphere. The numbers and global distribution of such organisms could have been greatly enhanced by an atmosphere containing significant quantities of H_2 . Each of the particular chemistries mediated by these organisms could thereby have a proportionately larger impact on the local or global environment than in the absence of a photosynthetic H_2 flux. In addition, H_2 itself can have an important impact on atmosphere and ocean chemistry. Hydrogen is “light” enough to escape to space, and in the process, carries electrons with it. The removal of electrons from our planet in this fashion would serve to facilitate the oxidation of our oceans and atmosphere from an initially reducing or neutral condition to the highly oxidized and oxygenated state that permits the existence of multi-celled life forms – including us! □

ANALYSIS OF THE TAGISH LAKE METEORITE

Sandra Pizzarello, Yongsong Huang, Luann Becker, Robert J. Poreda, Ronald A. Nieman, George Cooper, and Michael Williams

Carbonaceous meteorites provide an important record of organic compounds that were synthesized very early in the Solar System and delivered to the planets. Because a goal of NASA is to understand the origin and evolution of life, it is desirable to analyze a variety of such meteorites for their organic content.

The Tagish Lake meteorite fell in Canada in 2000 and was kept frozen until analysis. It may provide the most pristine material of its kind. Analyses have shown this carbonaceous meteorite to contain a suite of soluble organic compounds (~100 parts per million) that includes mono- and dicarboxylic acids, dicarboximides, pyridine carboxylic acids, a sulfonic acid, and both aliphatic and aromatic hydrocarbons. Surprisingly, some of the most abundant organic compounds of the well-studied Murchison meteorite were found to be very scarce in Tagish Lake. Amino acids, mono-carboxylic acids and amines are three orders of magnitude less abundant than in Murchison.

The difference between the two meteorites is also qualitative and very few species were found for each class of Tagish Lake compounds, contrary to Murchison's large isomerism. For example, while there is a series of straight chain carboxylic acids from formic to nonanoic acid, of the many possible branched isomers only isobutyric acid was detected. For amino acids and amines the list of identified compounds are few: glycine, alanine, α -amino iso- and n-butyric, and γ -amino butyric acids; and methyl, ethyl and isopropyl amines. In addition only the first two members of each series, e.g., acetic and formic acids, are present above trace levels. Also in contrast to Murchison, the abundance ratio of the first or second member of each series to the third ranges from approximately 10 to 100 (2 to 4 is typical Murchison).

The case of Tagish Lake sulfonic acids (organic sulfur compounds) is an extreme example as they were found to be represented in the meteorite by just methane sulfonic acid (MSA). MSA was found to be several times more abundant than in Murchison. Although other members of the series may ultimately be found it is apparent that the ratio of MSA to the other sulfonic acids would still be much higher in Tagish Lake than in Murchison. In Murchison sulfonic acids are present as a homologous series that extends to at least 4 carbons. MSA was found to be different from its homologs in having much higher amounts of carbon-13 and the heavier isotopes of sulfur. The present findings in Tagish Lake may be consistent with these isotopic differences.

The finding of just one suite of organic compounds matching those of Murchison and of some (but not all) the carbonaceous phases and compounds seen in other meteorites demonstrates the presence of distinct organic synthetic processes in primitive meteorites. It also implies that the more complex organic matter of heterogeneous meteorites may result from multiple, separate evolutionary pathways. □

COMPUTATIONAL MODELING OF REGULATORY NETWORKS IN CELLS

Andrew Pohorille, Stephen Bay, Pat Langley and Jeff Shrager

Understanding how an organism regulates its level of gene expression in response to external stimuli is a central problem in molecular biology. Although scientists understand the basic mechanisms through which DNA produces proteins and thus biochemical behavior, they have yet to determine most of the regulatory networks that control the degree to which each gene is expressed. This knowledge is necessary for understanding effects of space environments on cells and explaining interactions of organisms in ecosystems. Faulty cellular regulation is responsible for numerous diseases, of which cancer is the best known example. The BioLingua project, described here, provides interactive computational tools for biologists to build regulatory models using microarray data, which measure gene activity in terms of RNA expression levels in an organism. When the data are ambiguous, BioLingua relies on biological knowledge in the form of initial models and information about plausible causal relations between gene products.

The approach to discovering regulatory networks is based on linear causal models. In this approach, each variable is represented as a linear function of its direct causes plus an error term. Variables correspond to the expression levels of genes or measurements of external quantities. A regulatory network is represented as a graphical model, in which each variable is a node and causal influences are represented as arrows from the cause to the effect. The structure of the initial model can be obtained from constraints imposed by partial correlations between experimentally measured values of different variables. For example, a zero partial correlation between two variables means that they are connected through the third variable. A non-zero partial correlation implies that the variables are directly causally connected. The initial model is further refined through a search in the space of models consistent with biological knowledge to ensure that the predicted directions of changes in gene expression (up and down regulation) match those measured in experiments.

The methodology described above is illustrated in the example of photosynthesis regulation in Cyanobacteria, which are ubiquitous organisms in terrestrial, marine and freshwater ecosystems. Over 25% of the oxygen in the atmosphere is generated by Cyanobacteria. The model, shown in Figure 16, was generated on the basis of the recent microarray studies. It explains why Cyanobacteria exposed to high light conditions bleach and how this protects the organism. The model states that changes in light level modulate the expression of a protein dspA, which serves as a light sensor. This in turn regulates NBLR and NBLA proteins, which then reduce the number of phycobilisome (PBS) rods that absorb light. The reduction in PBS protects the organism's health by reducing absorption of light, which can be damaging at high levels. The sensor dspA impacts health through a second pathway by influencing an unknown response regulator RR, which in turn down regulates expression of the gene products psbA1, psbA2, and cpcB, which are all needed to form a functional photosystem. However, only the first protein was found to regulate the level of photosynthetic activity (Photo). High levels of photosynthetic activity would also damage the organism in high light conditions. □

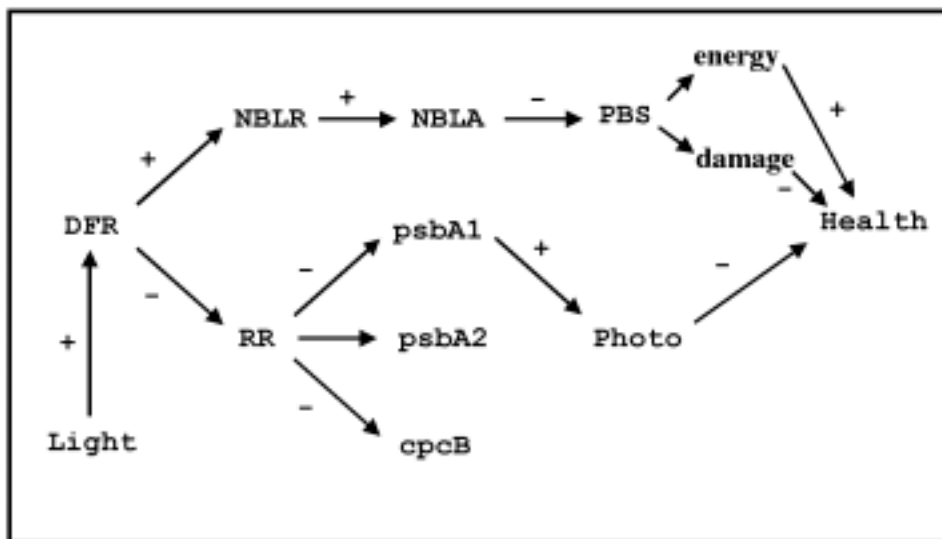


Figure 16: The proposed regulatory model of photosynthesis in Cyanobacteria.

A HIGH PERFORMANCE, LOW COST LINUX CLUSTER FOR GENOMICS

Karl Schweighofer and Rick Graul

In support of genomics research at NASA, the newly formed bioinformatics group (under the title of the NASA Center for Astroinformatics) has developed a Linux-based computer cluster configured with genomics tools. The cluster, also known as a Linux farm, is to serve as a test platform for developing genomics tools, and as an integral component of the newly formed bioinformatics infrastructure to support NASA specific research and missions. Such an infrastructure is justified due to the large number of scientists whose research employs the direct use of genomic information, and who are currently relying on outside resources to perform their analysis.

The Linux farm, called GRETEL, consists of 10 dual processor Pentium II 400 MHz processors, with an average of approximately 500 Mbytes of memory per node. The network topology employs a single network card in each node, each of which is connected to a local 100 Mbit switch. Of the 10 nodes, one is configured to be “Mother Superior”, and the others act as slaves, although each node has its own disk, operating system, and local copies of important databases. Mother Superior also acts as a web server, PBS batch server, and will allow remote logins for users who wish to have command line access to tools, or to develop their own code. Login access (ssh), and http requests are forwarded by a Linux-based firewall, which insulates the farm network from the outer ARC LAN. This is performed by network address translation, which masquerades the nodes so that each one has only a private network address. This allows for a high degree of reliability, since jobs started on the farm will continue even if the outer network experiences an interruption.

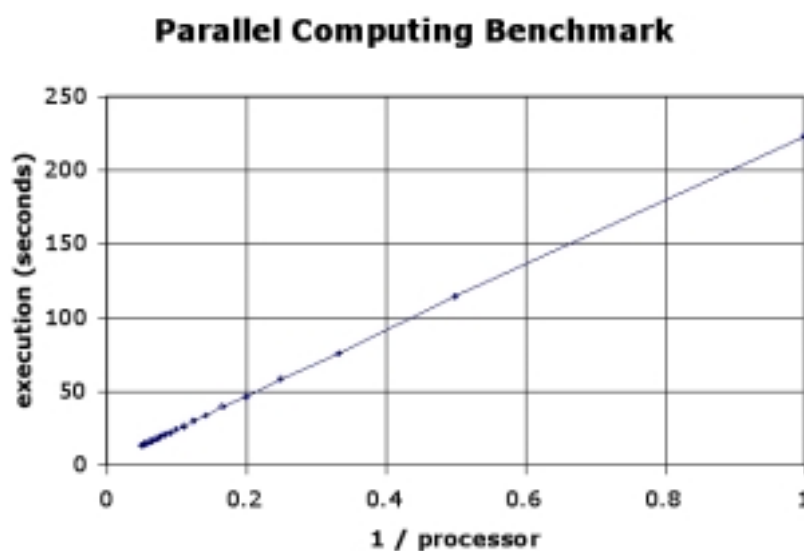


Figure 17: The linearity in the time for job completion with the number of processors.

Genomics tools are mostly centered around biological sequence analysis algorithms. In a typical analysis, a database of sequences is searched against a query sequence whose function may be unknown. If the search yields a set of “hits” from the database, and if these hits are similar in function, then one can infer the function of the unknown sequence by similarity. This type of search is highly parallel, since the comparison of the query with each sequence in the database is an independent calculation. Thus, an algorithm for splitting up the database, and submitting N searches to N nodes, is an effective parallelization method for these type of tools.

A benchmark of GRETEL was performed using a common sequence search algorithm known as HMMER, which operates under PVM (parallel virtual machine). HMMER consists of hidden markov modeling software, and the Pfam database, (a large set of HMM's trained on alignments of known protein domains). These domains may be used to infer the function of a protein, it's structure, or whether it is a known drug target, for example. For our benchmark we scored a single GPCR sequence against the entire Pfam database of about 3000 HMM's. Figure 17 shows the linearity in the time for job completion with the number of processors. Figure 18 is a photo of the Farm. This method of low cost computing is proving to be a valuable resource for scientists, given the enormous size of datasets associated with the human genome project. The resource is available at <http://genomics.arc.nasa.gov>. □



Figure 18: Photo of the Farm.